REMARKS/ARGUMENTS

Claims 53-70 are active. These claims find support in the original claims and disclosure. 95% and 98% identity as described in claims 53, 57 and 60 is disclosed at the top of page 8 and high stringency hybridization conditions of claim 63 at the bottom. Fragments are also described at the very bottom of page 8. No new matter has been introduced.

Restriction/Election

The Applicants previously elected with traverse **Group I,** claims 1-4, 9-16, and 25-29, directed to polynucleotides, and the species of the polynucleotide of **SEQ ID NO:1**. The requirement has been made FINAL. The Applicants understand that additional species will be rejoined and examined upon an indication of allowability for a generic claim reading on the elected species. The Applicants respectfully request that the claims of the nonelected group(s) or other withdrawn subject matter which depend from or otherwise include all the limitations of an allowed elected claim, be rejoined upon an indication of allowability for the elected claim, see MPEP 821.04.

Rejection--35 U.S.C. § 101

Claims 1 and 2 were rejected under 35 U.S.C. 101 as being directed to non-statutory subject matter. This rejection is moot in view of the cancellation of these claims.

Rejection--35 U.S.C. § 112, first paragraph

Claims 1 and 2 were rejected under 35 U.S.C. 112, first paragraph, as being directed to non-statutory subject matter. This rejection is moot in view of the cancellation of these claims. Polynucleotides that have at least 95% or 98% identity, or which hybridize under high stringency conditions, are expressly described on page 8 of the specification. The

disclosure of a percent identity provides the necessary written description. See Example 6 (hybridization) and Example 11 (percent identity) of the *Written Description Guidelines*, Rev. 1 (March 25, 2008). Accordingly, this rejection would not apply to the present claims.

Rejection--35 U.S.C. § 112, second paragraph

Claims 1 and 2 were rejected under 35 U.S.C. 101 as being indefinite. This rejection is moot in view of the cancellation of these claims.

Rejection--35 U.S.C. § 102

Claims 1 and 2 were rejected under 35 U.S.C. 102(b) as being anticipated by Khudyakov, et al., Virol. 88:8. This rejection is moot in view of the cancellation of these claims. It does not apply to the new claims which have been amended to remove the term "corresponds". Khudyakov is an old paper dated 1977 which does not disclose any nucleotide sequence, and specifically, does not disclose SEQ ID NO: 1.

Moreover, Khudyakov cannot inherently anticipate the polynucleotide of SEQ ID NO.1 because this is an engineered sequence different that natural cyanophage sequences which Khudyakov describes as containing D-bases. The SEQ ID NO: 1 is not the genomic sequence of Cyanophage S-2L *per se*, but an artificial sequence engineered to permit the heterologous expression of the cyanophage S-2L genes in a host cell. The inventors have engineered this sequence that provides for expression of Cyanophage S-2L genes in host cells despite the significant differences between the natural cyanophage sequences and the engineered sequence.

The natural genome of Cyanophage S-2L includes **2,6 diamino purine bases (D base)**, which is very unusual in living organisms. It is this unusual feature of cyanophage—the presence of D bases in the genome of Cyanophage S-2L—that has raised technical

problems in the implementation of standard sequencing and cloning techniques which are based on standard A, T, C, G nucleotide bases and not on D bases (see page 3 and 4 in the specification).

In order to overcome these problems, the inventors created an artificial sequence, namely SEQ ID NO.1, in which **D bases** have been **replaced** by standard **adenine (A bases)** over the whole Cyanophage S-2L genetic sequence. As disclosed in the specification on page 32, lines 21 to 30, this has been achieved by treating the genomic sequence with specific restriction enzymes and subsequent transformation (shot-gun cloning) in a bacterial host (*E. coli*), which is not the natural host for Cyanophage S-2L (*Synechococcus sp.*). As a result, SEQ ID NO.1 has made available the genome of cyanophage S-2L under the form of a polynucleotide sequence (A, T, C, G sequence) allowing the heterologous propagation and expression of cyanophage S-2L genome in a host cell.

Khudyakov did not disclose such engineered sequences nor did it suggest replacement of the D-bases found in the DNA by adenine, or provide a reasonable expectation of success for expression of heterologous expression of Cyanophage S-2L genes by such an engineered sequence. Accordingly, this rejection would not apply to the new claims.

Conclusion

This application presents allowable subject matter and the Examiner is respectfully requested to pass it to issue. The Examiner is kindly invited to contact the undersigned should a further discussion of the issues or claims be helpful.

Respectfully submitted,

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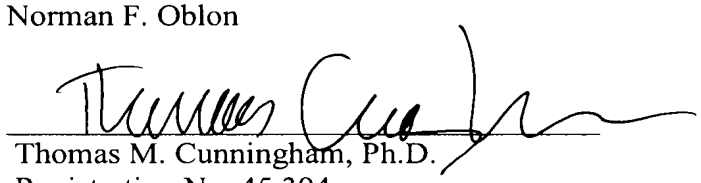

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